

## EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	1	((mitochondrial near3 respiratory) same (\$5array or \$4chip)) and @ad<"20020321"	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/11/24 11:04
L2	165	((mitochondrial) same (\$5array or \$4chip)) and @ad<"20020321"	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/11/24 11:04



# Sequence Revision History

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[Genome](#)
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[PMC](#)
[Taxonomy](#)
[OMIM](#)
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Find (Accessions, GI numbers or Fasta style SeqIds)



About Entrez

Show difference in



format

Gi	Version	Update Date
Entrez 565648	1	Aug 1 2006 12:46 PM
565648	1	Nov 9 1994 10:44 AM

Search for Genes

Entrez Gene provides gene-specific data for multiple taxa

Query= gi|565648|dbj|D26599.1|HUMPSH2 Homo sapiens mRNA for proteasome subunit HsC7-I, complete cds  
(762 letters)

Help|FAQ

Batch Entrez: Upload a file of GI or accession numbers to retrieve protein or nucleotide sequences

<gi|565648|dbj|D26599|HUMPSH2 Human mRNA for proteasome subunit HsC7-I  
Length = 762

Score = 1421 bits (717), Expect = 0.0  
Identities = 747/762 (98%)  
Strand = Plus / Plus

Check sequence revision history

How to create WWW links to Entrez

LinkOut

My NCBI (Cubby)

Related resources

BLAST

Reference sequence project

Entrez Gene

Clusters of orthologous groups

Protein reviews on the web

```

Query: 1  cggacctgcagccctggccttcgccaccatggagtagctcatcggtatccaaggcccg 6
          |||
Sbjct: 1  cggacctgcagccctggccttcgccaccatggagtagctcatcggtatccaaggcccg 6

Query: 61  actatgttcttgcgcctccgaccgggtggccgagcaatattgtccagatgaaggacg 1
          |||
Sbjct: 61  actatgttcttgcgcctccgaccgggtggccgagcaatattgtccagatgaaggacg 1

Query: 121  atcatgacaagatgtttaagatgagtgaagagatattactcctgtgtgtggagaggctg 1
          |||
Sbjct: 121  atcatgacaagatgtttaagatgagtgaagagatattactcctgtgtgtggagaggctg 1

Query: 181  gagacactgtacagtttgcagaatatattcagaaaaacgtgcaactttataagatgcgaa 2
          |||
Sbjct: 181  gagacactgtacagtttgcagaatatattcagaaaaacgtgcaactttataagatgcgaa 2

Query: 241  atggatatgaattgtctccacggcagcagctaacttcacacgccgaaacctgggtgact 3
          |||
Sbjct: 241  atggatatgaattgtctccacggcagcagctaacttcacacgccgaaacctgggtgact 3

Query: 301  gtcttcggagtcggaccccatatcatgtgaacctcctcctgggtggctatgatgagcatg 3
          |||
Sbjct: 301  gtcttcggagtcggaccccatatcatgtgaacctcctcctgggtggctatgatgagcatg 3

Query: 361  aagggccagcgtgtattacatggactacctggcagccttgccaaggcccttttgcag 4
          |||
Sbjct: 361  aagggccagcgtgtattacatggactacctggcagccttgccaaggcccttttgcag 4
  
```

```

Query:   421  cccacggctatggcgcttccctgactctcagtatcctcgaccgatactacacaccgacta 4
          |||
Sbjct:   421  cccacggctatggcgcttccctgactctcagtatcctcgaccgatactacacaccgacta 4

Query:   481  tctcacgtgagagggcagtggaactccttaggaaatgtctggaggagctccagaaacgct 5
          |||
Sbjct:   481  tctcacgtgagagggcagtggaactccttaggaaatgtctggaggagctccagaaacgct 5

Query:   541  tcatcctgaatctgccaaccttcagtggtcgaatcattgacaaaaatggcatccatgacc 6
          |||
Sbjct:   541  tcatcctgaatctgccaaccttcagtggtcgaatcattgacaaaaatggcatccatgacc 6

Query:   601  tggataacatttcccttccccaaacagggctcctaacatcatgtcctccctcccacttggc 6
          |||
Sbjct:   601  tggataacatttcccttccccaaacagggctcctaacatcatgtcctccctcccacttggc 6

Query:   661  agggaacnnnnnnnnngatggggtcctttannnnnnnctactcttttcaggcgcaactcttg 7
          |||
Sbjct:   661  agggaacttttttttgatggggtcctttattttttctactcttttcaggcgcaactcttg 7

Query:   721  ataaatggttaattcagaataaagggtgactatggatataatt 762
          |||
Sbjct:   721  ataaatggttaattcagaataaagggtgactatggatataatt 762

```

Score = 28.2 bits (14), Expect = 0.002  
Identities = 14/14 (100%)  
Strand = Plus / Minus

```
Query: 396 gccttggccaaggc 409
      |||||
Sbjct: 409 gccttggccaaggc 396
```

Score = 24.3 bits (12), Expect = 0.028  
Identities = 12/12 (100%)  
Strand = Plus / Minus

```
Query:  481  tctcacgtgaga  492
          |||||
Sbjct:  492  tctcacgtgaga  481
```

Lambda	K	H
1.37	0.711	1.31

Gapped			
Lambda	K	H	
1.37	0.711		1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2  
Number of Sequences: 1  
Number of Hits to DB: 191  
Number of extensions: 5  
Number of successful extensions: 5  
Number of sequences better than 10.0: 1  
Number of HSP's better than 10.0 without gapping: 1  
Number of HSP's gapped: 5  
Number of HSP's successfully gapped: 4  
Length of query: 762  
Length of database: 762  
Length adjustment: 9  
Effective length of query: 753  
Effective length of database: 753  
Effective search space: 567009  
Effective search space used: 567009  
X1: 8 (15.9 bits)  
X2: 15 (29.7 bits)  
X3: 25 (49.6 bits)  
S1: 8 (16.4 bits)  
S2: 8 (16.4 bits)

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